



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/605,708  
Source: IFWO  
Date Processed by STIC: 3/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/605,708

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☒ Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4 ☐ Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ Variable Length     Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7 ☐ Skipped Sequences  
    (OLD RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ Skipped Sequences  
    (NEW RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ Use of <220>     Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13 ☐ Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 03/25/2004

PATENT APPLICATION: US/10/605,708

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

1 <110> APPLICANT: GONG, Zhiyuan  
 2 LAM, Toong Jin  
 3 JU, Bensheng  
 4 XU, Yanfei  
 5 HE, Jiangyan  
 6 YAN, Tie  
 8 <120> TITLE OF INVENTION: CHIMERIC GENE CONSTRUCTS FOR GENERATION OF  
 9 FLUORESCENT TRANSGENIC ORNAMENTAL FISH  
 11 <130> FILE REFERENCE: 1781-0163P  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/605,708  
 C--> 14 <141> CURRENT FILING DATE: 2003-10-21  
 OK--> 17 <160> NUMBER OF SEQ ID NOS: 24  
 19 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2480  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Danio rerio  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (90)..(1586)  
 30 <220> FEATURE:  
 W--> 31 <221> NAME/KEY: primer bind  
 32 <222> LOCATION: (66)..(85)  
 33 <223> OTHER INFORMATION: CK2  
 35 <220> FEATURE:  
 W--> 36 <221> NAME/KEY: primer\_bind  
 37 <222> LOCATION: (97)..(120)  
 38 <223> OTHER INFORMATION: CK1  
 40 <220> FEATURE:  
 W--> 41 <221> NAME/KEY: polyA signal  
 42 <222> LOCATION: (24467)..(2451)  
 44 <400> SEQUENCE: 1  
 45 ctctcctttg tgagcaacct cctccactca ctctctctc agagagcact ctctgtacctc 60  
 46 cttctcagca actcaaagac acaggcatc atg tca acc agg tct atc tct tac 113  
 47 Met Ser Thr Arg Ser Ile Ser Tyr  
 48 1 5  
 50 tcc agc ggt ggc tcc atc agg agg ggc tac acc agc cag tca gcc tat 161  
 51 Ser Ser Gly Gly Ser Ile Arg Arg Gly Tyr Thr Ser Gln Ser Ala Tyr  
 W--> 52 10 15 20

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 1-5)

⌞ please see item #  
 3 on error summary  
 sheet.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

*Add space*

```

54 gca gta cct gcc ggc tct acc agg atg agc tca gtg acc agt gtc agg 209
55 Ala Val Pro Ala Gly Ser Thr Arg Met Ser Ser Val Thr Ser Val Arg
W--> 56 25 30 35 40
58 aga tct ggt gtg ggt gcc agc cca ggc ttc ggt gcc ggt ggc agc tac 257
59 Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr
W--> 60 45 50 55
62 agc ttt agc agc agc agc atg ggt gga ggc tat gga agt ggt ctt ggt 305
63 Ser Phe Ser Ser Ser Ser Met Gly Gly Gly Tyr Gly Ser Gly Leu Gly
W--> 65 gga ggt ctc ggt ggg ggc atg ggc ctt cgt tgc ggg ctt ctt atc aca 353
66 Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr
W--> 67 75 80 85
69 gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc 401
70 Ala Val Thr Val Asn Gln Asn Leu Leu Ala Pro Leu Asn Leu Glu Ile
W--> 71 90 95 100
73 gac ccc aca att caa gac gtc cgc act tca gag aaa gag cag att aag 449
74 Asp Pro Thr Ile Gln Ala Val Arg Thr Ser Glu Lys Glu Gln Ile Lys
W--> 75 105 110 115 120
77 acc ttc aac aac cgc ttc gct ttc ctc atc gac aaa gtg cgc ttc ctg 497
78 Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile Asp Lys Val Arg Phe Leu
W--> 79 125 130 135
81 gaa cag cag aac aag atg ctt gag acc aaa tgg agt ctt ctc caa gaa 545
82 Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Glu
W--> 83 140 145 150
85 cag aca acc aca cgt tcc aac atc gat gcc atg ttt gag gca tac atc 593
86 Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile
W--> 87 155 160 165
89 tct aac ctg cgc aga cag ctc gat gga ctg gga aat gag aag atg aag 641
90 Ser Asn Leu Arg Arg Gln Leu Asp Gly Leu Gly Asn Glu Lys Met Lys
W--> 91 170 175 180
93 ctg gag gga gag ctg aag aac atg cag ggc ctg gtt gag gac ttc aag 689
94 Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe Lys
W--> 95 185 190 195
97 aac aag tac gag gat gag atc aac aag cgt gct tcc gta gag aat gag 737
98 Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn Glu
W--> 99 205 210 215
101 ttt gtc ctg ctc aag aag gat gtt gat gca gcc tac atg aac aag gtt 785
102 Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys Val
W--> 103 220 225 230
105 gag ctt gaa gcc aag gtt gat gct ctt cag gat gag atc aac ttc ctc 833
106 Glu Leu Glu Ala Lys Val Asp Ala Leu Gln Asp Glu Ile Asn Phe Leu
W--> 107 235 240 245
109 agg gca gtc tac gag gct gaa ctc cgg gag ctc cag tct cag atc aag 881
110 Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Gln Ile Lys
W--> 111 250 255 260
113 gac aca tct gtt gtt gta gaa atg gac aac agc aga aac ctg gat atg 929
114 Asp Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met
W--> 115 265 270 275
117 gac tcc atc gtg gct gaa gtt cgc gct cag tat gaa gac atc gcc aac 977
118 Asp Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn

```

*Invalid  
nucleotide  
code*

*SAME ERROR*

*SAME ERROR*

*SAME ERROR*

*SAME ERROR*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004  
TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt  
Output Set: N:\CRF4\03252004\J605708.raw

*SAME errors*  
✓

```

W--> 119          285          290          295
121 cgc agc cgt gcc gag gca gag agc tgg tac aaa cag aag ttt gag gag 1025
122 Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Gln Lys Phe Glu Glu
W--> 123          300 300 SAME error 305 305          310 310
E--> 125 atg cag agc acc ggt cag tat ggt gat gac ctc cgc tca aca aag 1073
126 Met Gln Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys
W--> 127          315 315 SAME error 320 320          325 325
E--> 129 gct gag att ggt gaa ctc aac cgc atg atc gcc cgc ctg cag aac gag 1121
W--> 130 Ala Glu Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Gln Asn Glu
W--> 131          330 330          335 335          340 340
E--> 133 atc gat gct gtc aag gca cag cgt gcc aac ttg gag gct cag att gct 1169
W--> 134 Ile Asp Ala Val Lys Ala Gln Arg Ala Asn Leu Glu Ala Gln Ile Ala
W--> 135          345 345 INVALID code 350 350          355 355          360 360
E--> 137 gag gct gaa gag cgt gga gag ctg gca gtg aag gat gcc aag ctc cgc 1217
138 Glu Ala Glu Glu Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg
W--> 139          360          365 365          370 370          375 375
E--> 141 atc agg gag ctg gag gaa get ctt cag agg gcc aag caa gac atg gcc 1265
W--> 142 Ile Arg Glu Leu Glu Glu Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
W--> 143          380 380          385 385          390 390
E--> 145 cgc cag gtc cgc gag tac cag gag ctc atg aac gtc aaa ttg gct ctg 1313
146 Arg Gln Val Arg Glu Tyr Gln Gln Leu Met Asn Val Lys Leu Ala Leu
W--> 147          395 395          400 400          405 405
149 gac att gag atc gcc acc tac agg aaa ctg ttg gaa gga gag gag agc 1361
150 Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser
W--> 151          410 410          415 415          420 420
E--> 153 aga ctg tcc agc ggt gga gct caa gct acc att cat gtt cag gag acc 1409
W--> 154 Arg Leu Ser Ser Gly Gly Ala Gln Ala Thr Ile His Val Gln Gln Thr
W--> 155          425 425          430 430          435 435          440 440
157 tcc gga ggt gtt tca tct ggt tat ggt ggt agc gcc tct ggt ttc gcc 1457
158 Ser Gly Gly Val Ser Ser Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly
W--> 159          440          445 445          450 450          455 455
161 tac agc agt gcc ttc agc agt ggt ggg tca gga tac ggt agt gga tca 1505
162 Tyr Ser Ser Gly Phe Ser Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser
W--> 163          460 460          465 465          470 470
165 gga ttc ggt tct gga tca ggg tat ggt gga gcc tcc atc agc aaa acc 1553
166 Gly Phe Gly Ser Gly Ser Gly Tyr Gly Gly Ser Ile Ser Lys Thr
W--> 167          475 475          480 480          485 485
169 agt gtc acc acc gtc agc agt aaa cgc tat taa ggagaagccc gcccaaacc 1606
170 Ser Val Thr Thr Val Ser Ser Lys Arg Tyr
W--> 171          490 490          495 495
173 ccagccgaca cagtttccaa ccttccttac ctgcaactag atcccttctg aaccttctta 1666
175 cgactcaaac catctatggt gctatatattt agccagacag ctgtcccctg ttaatgagga 1726
177 gatgtggacg atgattttta aagtacaaaa taagttttag attgttctgt gtgttgatgg 1786
179 tagttaccgc tatcatgcat ctccgtgtctg gtggtgtcac tgccatttta aatcatcaac 1846
181 ccaactacac taaaacgata ccaggaagaa tcgtgctcca agccactgaa tagtcttatt 1906
183 tctgactaga tatgtacagg gaaagtgaga cacatagaaa ccactgtaac ctacgtagta 1966
185 ctatggtttc actggatcag ggggtgtgcta tacaagttcc tgaatgtctt gtttgaatgt 2026
187 tttgtgctgt tacaagctcc ctgctgtagt tttgtgact aatctgactt ttgtcatttt 2086
189 gctatggctg tcagagttgg tttacctatt ttctataaaa tgtatatggc agtcagccaa 2146

```

*INVALID Amino Acid Code*  
*INVALID Amino Acid Code*

*see item # 3 on error summary sheet.*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set : N:\CRF4\03252004\J605708.raw

191 taactgatga caattgcttg tgggctacta atgtccagtt acctcacatt caagggagat 2206  
 193 ctgttacagc aaaaaacagg cacaatggga tttatgtgga ccatccctcc ttaaccttgt 2266  
 195 gtactttccg tgttggaagt ggtgactgta ctgccttaca cattcccctg tattcaactg 2326  
 197 gcttccagag catattttac atccccggtt ataaatggaa aatgcaagaa aactgaaaca 2386  
 199 atgttcaacc agattttattt ggtattgatt gacgagacac caacttgaaa tttgaataca 2446  
 201 ataaatctga gaccacaaaa aaaaaaaaaa aaaa 2480

204 &lt;210&gt; SEQ ID NO: 2

205 &lt;211&gt; LENGTH: 498

206 &lt;212&gt; TYPE: PRT

207 &lt;213&gt; ORGANISM: Danio rerio

209 &lt;400&gt; SEQUENCE: 2

210 Met Ser Thr Arg Ser Ile Ser Tyr Ser Ser Gly Gly Ser Ile Arg Arg  
 211 1 5 10 15  
 213 Gly Tyr Thr Ser Gln Ser Ala Tyr Ala Val Pro Ala Gly Ser Thr Arg  
 214 20 25 30  
 216 Met Ser Ser Val Thr Ser Val Arg Arg Ser Gly Val Gly Ala Ser Pro  
 217 35 40 45  
 219 Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Ser Met Gly  
 220 50 55 60  
 222 Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly  
 223 65 70 75 80  
 225 Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Asn Leu Leu  
 226 85 90 95  
 228 Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Ala Val Arg Thr Ser  
 229 100 105 110  
 231 Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile  
 232 115 120 125  
 234 Asp Lys Val Arg Phe Leu Glu Asn Lys Met Leu Glu Thr Lys Trp Ser  
 235 130 135 140  
 237 Leu Leu Glu Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala  
 238 145 150 155 160  
 240 Tyr Ile Ser Asn Leu Arg Arg Leu Asp Gly Leu Gly Asn Glu Lys Met  
 241 165 170 175  
 243 Lys Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe  
 244 180 185 190  
 246 Lys Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn  
 247 195 200 205  
 249 Glu Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys  
 250 210 215 220  
 252 Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asp Glu Ile Asn Phe Leu  
 253 225 230 235 240  
 255 Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Ile Lys Asp  
 256 245 250 255  
 258 Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met Asp  
 259 260 265 270  
 261 Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn Arg  
 262 275 280 285  
 264 Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Lys Phe Glu Glu Met Gln  
 265 290 295 300

Found 484

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

```

267 Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu
268 305 310 315 320
270 Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Asn Glu Ile Asp Ala
271 325 330 335
273 Val Lys Ala Arg Ala Asn Leu Glu Ala Gln Ile Ala Glu Ala Glu Glu
274 340 345 350
276 Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg Ile Arg Glu Leu
277 355 360 365
279 Glu Glu Ala Leu Gln Arg Ala Lys Asp Met Ala Arg Gln Val Arg Glu
280 370 375 380
282 Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu Asp Ile Glu Ile Ala
283 385 390 395 400
285 Thr Tyr Arg Lys Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly
286 405 410 415
288 Gly Ala Gln Ala Thr Ile His Val Gln Thr Ser Gly Gly Val Ser Ser
289 420 425 430
291 Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser
292 435 440 445
294 Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly Ser Gly Ser
295 450 455 460
297 Gly Tyr Gly Gly Gly Ser Ile Ser Lys Thr Ser Val Thr Thr Val Ser
298 465 470 475 480

```

--> 300 Ser Lys Arg Tyr - see pg. 4

611 <210> SEQ ID NO: 6

612 <211> LENGTH: 319

613 <212> TYPE: PRT

614 <213> ORGANISM: Danio rerio

--> 616 <400> SEQUENCE: ②-6

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617 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys
618 1 5 10 15
619 Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala
620 20 25 30
621 Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg
622 35 40 45
623 Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
624 50 55 60
625 Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro
626 65 70 75 80
627 His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
628 85 90 95
629 Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
630 100 105 110
631 Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
632 115 120 125
633 Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
634 130 135 140
635 Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
636 145 150 155 160
637 Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn

```

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Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

```

638          165          170          175
639 Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
640          180          185          190
641 Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
642          195          200          205
643 Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
644          210          215          220
645 Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
646 225          230          235          240
647 Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
648          245          250          255
649 Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
650          260          265          270
651 Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
652          275          280          285
653 Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
654          290          295          300
655 Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
656 305          310          315

```

1130 &lt;210&gt; SEQ ID NO: 22

1131 &lt;211&gt; LENGTH: 2054

1132 &lt;212&gt; TYPE: DNA

1133 &lt;213&gt; ORGANISM: Danio rerio

1135 &lt;220&gt; FEATURE:

V--&gt; 1136 &lt;221&gt; NAME/KEY: TATA signal

1137 &lt;222&gt; LOCATION: (1983)..(1989)

1139 &lt;220&gt; FEATURE:

1140 &lt;221&gt; NAME/KEY: enhancer

1141 &lt;222&gt; LOCATION: (142)..(148)

1142 &lt;223&gt; OTHER INFORMATION: E-box, canntg

1144 &lt;220&gt; FEATURE:

1145 &lt;221&gt; NAME/KEY: enhancer

1146 &lt;222&gt; LOCATION: (452)..(457)

1147 &lt;223&gt; OTHER INFORMATION: &lt;223&gt; E-box, canntg

1149 &lt;220&gt; FEATURE:

1150 &lt;221&gt; NAME/KEY: enhancer

1151 &lt;222&gt; LOCATION: (1095)..(1100)

1152 &lt;223&gt; OTHER INFORMATION: E-box, canntg

1154 &lt;220&gt; FEATURE:

1155 &lt;221&gt; NAME/KEY: enhancer

1156 &lt;222&gt; LOCATION: (1278)..(1283)

1157 &lt;223&gt; OTHER INFORMATION: E-box, canntg

1159 &lt;220&gt; FEATURE:

1160 &lt;221&gt; NAME/KEY: enhancer

1161 &lt;222&gt; LOCATION: (1362)..(1367)

1162 &lt;223&gt; OTHER INFORMATION: E-box, canntg

1164 &lt;220&gt; FEATURE:

1165 &lt;221&gt; NAME/KEY: enhancer

1166 &lt;222&gt; LOCATION: (1385)..(1390)



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

1167 <223> OTHER INFORMATION: E-box, canntg  
 1169 <220> FEATURE:  
 1170 <221> NAME/KEY: enhancer  
 1171 <222> LOCATION: (523)..(532)  
 1172 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1174 <220> FEATURE:  
 1175 <221> NAME/KEY: enhancer  
 1176 <222> LOCATION: (606)..(615)  
 1177 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1179 <220> FEATURE:  
 1180 <221> NAME/KEY: enhancer  
 1181 <222> LOCATION: (697)..(706)  
 1182 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1184 <220> FEATURE:  
 1185 <221> NAME/KEY: enhancer  
 1186 <222> LOCATION: (1490)..(1499)  
 1187 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1189 <220> FEATURE:  
 1190 <221> NAME/KEY: enhancer  
 1191 <222> LOCATION: (1640)..(1649)  
 1192 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1194 <220> FEATURE:  
 1195 <221> NAME/KEY: enhancer  
 1196 <222> LOCATION: (1956)..(1965)  
 1197 <223> OTHER INFORMATION: Potential MEF2 binding site, yta(w)4tar  
 1199 <220> FEATURE:  
 1200 <223> OTHER INFORMATION: Transcription start site at residue 2012.  
 1202 <220> FEATURE:  
 W--> 1203 <221> NAME/KEY: primer bind  
 1204 <222> LOCATION: (2032)..(2054)  
 1205 <223> OTHER INFORMATION: M2  
 1207 <220> FEATURE:  
 W--> 1208 <221> NAME/KEY: misc difference  
 1209 <222> LOCATION: (2027)..(2054)  
 1210 <223> OTHER INFORMATION: Identical to the 5' MLC2f cDNA

E--> 1211 <409> 22  
 1007 1212 tgcatgcctg gcaggtccac tctagaggac tactagtcac atgcgattct gaacaatgct 60  
 1213 ggaatgagcc accaactcat ccagtgatt accctacact gggaaacacc caaatctgtc 120  
 1214 tgttatattt gtgcatatac attagattag aagctgtcac tgcggtggtta ccttttcaaa 180  
 W--> 1215 ttgataacct aaaagtatat attagtgcct tttaggtact aatataatcc cttgagggtt 240  
 W--> 1216 tcatttgga aggtaccacc ccagtgacag aaatctggag cttatttaac aaaataactt 300  
 W--> 1217 tatttatatg ttattgaaaa atattaaata agcaaaacaa tggaaaaaaa ttagttcaaa 360  
 W--> 1218 atttagcttt atttaaattg ttttatcttt aatatagctg ttttaataaat ctgttttggt 420  
 W--> 1219 actgagagat ggagaaaaat attcattttc ctgtaattat ctgtttttct aggtactgta 480  
 W--> 1220 caagcaggag caaaacaagc cgacagactc gggaatgcac aacaaactca agggggggcaa 540  
 W--> 1221 gagagcaagg agcgtctcaag attgttttagc ctgccttccc aaaaaaaaac tgtcttaagc 600  
 W--> 1222 caaccactca gagggctgta gtgtgctgac cgtgcttgct cacagggcag cttcccacaa 660  
 W--> 1223 gtgagggtcat aggtcgatcg gcagagagag atgggcatgg ccatgtggac ggggtgtggtg 720  
 W--> 1224 actatactag gaaaagcatt aaaacctatt aagacaccag aacgtcctct tatatatcag 780

OK  
 this  
 is due  
 to above  
 error.

Invalid  
 Numeric  
 identifier

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:31

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

W--> 1225 tcattggctc aaaaatctct ggattgaaat atccaacaag taatcctgca agataagcca 840  
 W--> 1226 ggagggagtt gcgtccctt tagactcagt atgtgattgt atgaagctca aacagtccct 900  
 W--> 1227 gtggacagct tgaattcaat tcgccacaga ttttatgcag cggatgcca tccagttgca 960  
 W--> 1228 ttttaaatta atatttttaa taggaagcta tcagtacact ctcagaaata aatgggccgc 1020  
 W--> 1229 aggtacatat ttgtacttaa agggtcata aaaaatttta agagaaacac tttgtactt 1080  
 W--> 1230 tattatggac ctttaaggta caaattttta ctacgcctt ttatttctga gagtgaagct 1140  
 W--> 1231 atgataacgg tccaaaaact actacacca caaatttata aacaggggaa aatcaagaga 1200  
 W--> 1232 atttgtaggt tgtaattttt ttgttgcaat caattttgtg actaaaatat tattttaata 1260  
 W--> 1233 taaatgcacc aaaatacatt gcctatatc aaaaatgggt gtactcaatt actctaagca 1320  
 W--> 1234 aaataatgct aatcttaaac aattttggaa acaggatata aaattagtct aaagaaagaa 1380  
 W--> 1235 aacagtgact gatgaattag acaagaaaaa tattttgggt accacagctg ttccttatgc 1440  
 W--> 1236 ctcaaatttc tcttcattgag ggtccaacat catctaaaaa ctgggaaaaa ggggtaatta 1500  
 W--> 1237 atggcacctc acagtcactg aagtgaccgg agagagagag agagagagag agtgcgta 1560  
 W--> 1238 ggggcacttg aaccgaaatc ttacagcatc ttcgattagg gctgatttga aataagggtt 1620  
 W--> 1239 ccagggcggtg aacaaatatg aacaacataa ccatcaggat ctatcactgc aaccctcccc 1680  
 W--> 1240 gtattgatct gctgctaata taactttagg ggctacagct cattcatttc aaattgagtt 1740  
 W--> 1241 tacgtcccca tgccttatt agacaacggg agacatgcag gccgctgcca tcagtatcag 1800  
 W--> 1242 attcatccca ttccaagact ccaatagcta tttctgagca ctgtaagatg atagtacatc 1860  
 W--> 1243 ccagccgggtg tccctccatc actttccccc tacctcatag tttttcctct ttctctctcg 1920  
 W--> 1244 gtctgctatt tcccaaact cacttaaggt tgggtctata attagcaagg ggccttcgtc 1980  
 W--> 1245 agtatataag cccctcaagt acaggacact acgcggcttc agacttctct tcttgatctt 2040  
 W--> 1246 ~~attagacttc~~ acac 2054  
 OK -> 1250 <400> SEQUENCE:  
 E -> 1250  
 OK -> 1250 <210> SEQ ID NO: 23

↑  
 OK,  
 this is  
 due to  
 above  
 error  
 ON previous  
 page.

## VARIABLE LOCATION SUMMARY

DATE: 03/25/2004

PATENT APPLICATION: US/10/605,708

TIME: 09:07:32

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

Use of n's or Xaa's (NEW RULES):

*Error Explanation: ✓*

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:17; N Pos. 10

<210> 17  
<211> 10  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide for linker used in linker-mediated PCR

<220> ← please insert <222>, to show "N" location.

<223> n is a dideoxycytidine

<400> 17  
gaattcaagn

↑ please see error explanation on  
page 9.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:32

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:36 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:41 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:73 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:97 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:109 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:125 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:129 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:130 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:133 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3 ✓  
L:134 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:137 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:141 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:142 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:145 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:153 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:154 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:32

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:300 M:252 E: No. of Seq. differs, <211> LENGTH:Input:498 Found:484 SEQ:2 ✓  
L:313 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:323 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:508 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:513 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:606 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:616 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:2 ✓  
L:665 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:674 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:724 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:771 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:850 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:855 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:873 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:891 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:896 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:927 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:932 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:966 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:17  
L:966 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:17  
L:966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:1005 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:1010 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:1015 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:1019 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:1068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:1136 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:1203 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:1208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:1211 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER ✓  
L:1215 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1216 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1217 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1218 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1219 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1220 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1221 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1222 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1223 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1224 M:259 W: Allowed number of lines exceeded, <223> Other Information:

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/605,708

DATE: 03/25/2004

TIME: 09:07:32

Input Set : D:\GLOF007USC1.txt

Output Set: N:\CRF4\03252004\J605708.raw

L:1225 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1226 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1227 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1228 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1229 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1230 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1231 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1232 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1233 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1234 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1235 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1236 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1237 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1238 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1239 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1240 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1241 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1242 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1243 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1244 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1245 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1246 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1250 M:200 E: Mandatory Header Field missing, <400> is required.  
L:1250 M:301 E: (44) No Sequence Data was Shown, SEQ ID:22  
L:1250 M:252 E: No. of Seq. differs, <211> LENGTH: Input:2054 Found:0 SEQ:22  
L:1250 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:23  
L:17 M:203 E: OK No. of Seq. differs, <160> Number Of Sequences: Input (24) Counted (23)